CLAIMS

We claim:

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- 1. A method for generating a secondary library of scaffold protein variants comprising:
 - a) receiving a library of primary sequences generated utilizing an alignment program;
- b) generating a probability distribution table of amino acid residues in a plurality of variant positions from said primary sequences;
- c) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences; and
 - d) computationally ranking said secondary library.
- 2. A method according to claim 1, wherein said alignment program is a sequence alignment program.
- 15 3. A method according to claim 1, wherein said alignment program is a structural alignment program.
 - 4. A method according to claim 1 further comprising synthesizing a plurality of said secondary sequences.
 - 5. A method according to claim 4 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.
- 6. A method according to 5 wherein said pooled oligonucleotides are added in equimolar amounts.
 - 7. A method according to claim 5 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the mutation.
- 30 8. A method according to claim 6 wherein said pooled oligonucleotides are pooled in relative amounts.